

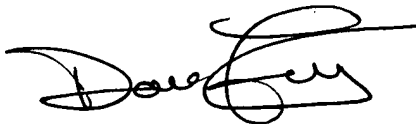
REMARKS

In response to the Notice of Defective Response, a copy of the substitute sequence listing in computer readable form is attached hereto. The content of the paper copy of the sequence listing and the copy of the sequence listing in computer readable form is the same, and includes no new matter.

It is believed that by submitting the present amendment and the sequence listing diskette, the application now fully complies with the requirements of 37 CFR §§ 1.821-1.825. Applicants respectfully solicit issuance of the patent.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit any excess fees to such deposit account.

Respectfully submitted,
KEIL & WEINKAUF



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Reg. No. 48,692

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Washington, D.C. 20036
(202)659-0100

DCL/kas

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SEQUENCE LISTING

<110> Kock, Michael
 Hoeger, Thomas
 Kroeger, Burkhard
 Otterbach, Bernd
 Lubisch, Wilfried
 Lemaire, Hans-Georg

<120> Poly (ADP-ribose) polymerase-gene

<130> 0050/49100

<140> US 09/701,586

<141> 1999-06-04

<150> PCT/EP99/03889

<151> 1999-06-04

<160> 33

<170> PatentIn/WordPerfect

<210> 1

<211> 1843

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3)...(1715)

<223> product is Poly ADP Ribose Polymerase; from brain tissue

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gac aag caa gat gaa tct gtg aag gcc ttg ctg tta aag ggc aaa gct 239
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cta cat tgt gcc ttg cgc ccc ctt gac cat gaa agt tac gag ttc aaa 1103
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 Tyr Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu
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Leu Lys Val Gln Phe Asn Phe Leu Gln Leu Trp	
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<212> PRT

<213> Homo sapiens

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Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala Pro
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Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys Glu		
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Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys Ile		
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Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln Leu		
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<210> 3

<211> 2265

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (242)...(1843)

<223> product is Poly ADP Ribose Polymerase; from uterus tissue

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tctccctaatt tcacgcctga ggctcatgga gagttgctag acctgggact gccctgggag	180
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Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser	
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Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg	
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Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn	
65 70 75	
aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc ttc	526
Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe	
80 85 90 95	
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Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys	
100 105 110	
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His	Phe	Tyr	Thr	Val	Ile	Pro	His	Asn	Phe	Gly	His	Ser	Gln	Pro	Pro	
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ccc	atc	aat	tcc	cct	gag	ctt	ctg	cag	gcc	aag	aag	gac	atg	ctg	ctg	1102
Pro	Ile	Asn	Ser	Pro	Glu	Leu	Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	
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gtg	ctg	gcg	gac	atc	gag	ctg	gcc	cag	gcc	ctg	cag	gca	gtc	tct	gag	1150
Val	Leu	Ala	Asp	Ile	Glu	Leu	Ala	Gln	Ala	Leu	Gln	Ala	Val	Ser	Glu	
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cag	gag	aag	acg	gtg	gag	gag	gtg	cca	cac	ccc	ctg	gac	cga	gac	tac	1198
Gln	Glu	Lys	Thr	Val	Glu	Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	
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cag	ctt	ctc	aag	tgc	cag	ctg	cag	ctg	cta	gac	tct	gga	gca	cct	gag	1246
Gln	Leu	Leu	Lys	Cys	Gln	Leu	Gln	Leu	Leu	Asp	Ser	Gly	Ala	Pro	Glu	
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Cys	Pro	Thr	Leu	Gln	His	Ile	Trp	Lys	Val	Asn	Gln	Glu	Gly	Glu	Glu	
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Asp	Arg	Phe	Gln	Ala	His	Ser	Lys	Leu	Gly	Asn	Arg	Lys	Leu	Leu	Trp	
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His	Gly	Thr	Asn	Met	Ala	Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	
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Arg	Ile	Met	Pro	His	Ser	Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	
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Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro			
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Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro			
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<212> PRT

<213> Homo sapiens

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Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn Asn	65	70	75
Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe Thr	85	90	95
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Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu Asp Glu	145	150	155
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Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser His	245	250	255
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 325 330 335

Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg Cys
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Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu Asp
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Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp His
 370 375 380

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Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
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Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys Gly
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Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg
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Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro Pro
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Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro Thr
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Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro Gln
 485 490 495

Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser Gln
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Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr Leu
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<210> 5

<211> 2265

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (221)...(1843)

<223> product is Poly ADP Ribose Polymerase; from uterus tissue

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gcgcacacaa ccaggccggg tggcagccag gacctctccc atg tcc ctg ctt ttc 235
Met Ser Leu Leu Phe
1 5

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Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro
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gag aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc 331
Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg
25 30 35

tcc acc gct gag gcc ctc aag gcc ata ccc gca gag aag cgc ata atc 379
Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile
40 45 50

cgc gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg 427
Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val
55 60 65

tat gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac 475
Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn
70 75 80 85

aac aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc 523
Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe
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ttc acc tgc tgg aac cgc tgg ggc cgt gtg gga gag gtc ggc cag tca 571
Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser
105 110 115

aag atc aac cac ttc aca agg cta gaa gat gca aag aag gac ttt gag 619
Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu
120 125 130

aag aaa ttt cgg gaa aag acc aag aac aac tgg gca gag cgg gac cac 667
Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His
135 140 145

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Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu	
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Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg	
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Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln	
185 190 195	
aag ctc atc act aac atc ttc agc aag gag atg ttc aag aac acc atg	859
Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met	
200 205 210	
gcc ctc atg gac ctg gat gtg aag aag atg ccc ctg gga aag ctg agc	907
Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser	
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aag caa cag att gca cgg ggt ttc gag gcc ttg gag gcg ctg gag gag	955
Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu	
230 235 240 245	
gcc ctg aaa ggc ccc acg gat ggt ggc caa agc ctg gag gag ctg tcc	1003
Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser	
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Ser His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro	
265 270 275	
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Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu	
280 285 290	
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Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser	
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Glu Gln Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp	
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Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro	
330 335 340	
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Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His	
345 350 355	
agg tgc cct aca ctt caa cac atc tgg aaa gta aac caa gaa ggg gag	1339

tgt ggg gcc cac cat gtc ggc tac atg ttc ctg ggt gag gtg gcc ctg	1579
Cys Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu	
440 445 450	
ggc aga gag cac cat atc aac acg gac aac ccc agc ttg aag agc cca	1627
Gly Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro	
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Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp	
470 475 480 485	
ccg acc cag gac act gag ttg gag ctg gat ggc cag caa gtg gtg gtg	1723
Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val	
490 495 500	
ccc cag ggc cag cct gtg ccc tgc cca gag ttc agc agc tcc aca ttc	1771
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tcc cag agc gag tac ctc atc tac cag gag agc cag tgt cgc ctg cgc	1819
Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg	
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tac ctg ctg gag gtc cac ctc tga gtgccccgcc tgtcccccg ggtcctgcaa	1873
Tyr Leu Leu Glu Val His Leu	
535 540	

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2265

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Glu	Asp	Pro	Phe	Arg	Ser	Thr	Ala	Glu	Ala	Leu	Lys	Ala	Ile	Pro	Ala
	35						40					45			

Glu	Lys	Arg	Ile	Ile	Arg	Val	Asp	Pro	Thr	Cys	Pro	Leu	Ser	Ser	Asn
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Pro	Gly	Thr	Gln	Val	Tyr	Glu	Asp	Tyr	Asn	Cys	Thr	Leu	Asn	Gln	Thr
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Asn	Ile	Glu	Asn	Asn	Asn	Asn	Lys	Phe	Tyr	Ile	Ile	Gln	Leu	Leu	Gln
			85						90					95	

Asp	Ser	Asn	Arg	Phe	Phe	Thr	Cys	Trp	Asn	Arg	Trp	Gly	Arg	Val	Gly
		100						105				110			

Glu	Val	Gly	Gln	Ser	Lys	Ile	Asn	His	Phe	Thr	Arg	Leu	Glu	Asp	Ala
	115						120					125			

Lys	Lys	Asp	Phe	Glu	Lys	Lys	Phe	Arg	Glu	Lys	Thr	Lys	Asn	Asn	Trp
	130					135					140				

Ala	Glu	Arg	Asp	His	Phe	Val	Ser	His	Pro	Gly	Lys	Tyr	Thr	Leu	Ile
145					150					155				160	

Glu	Val	Gln	Ala	Glu	Asp	Glu	Ala	Gln	Glu	Ala	Val	Val	Lys	Val	Asp
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Arg	Gly	Pro	Val	Arg	Thr	Val	Thr	Lys	Arg	Val	Gln	Pro	Cys	Ser	Leu
		180						185					190		

Asp	Pro	Ala	Thr	Gln	Lys	Leu	Ile	Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met
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195	200	205
Phe Lys Asn Thr Met Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro 210 215 220		
Leu Gly Lys Leu Ser Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu 225 230 235 240		
Glu Ala Leu Glu Glu Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser 245 250 255		
Leu Glu Glu Leu Ser Ser His Phe Tyr Thr Val Ile Pro His Asn Phe 260 265 270		
Gly His Ser Gln Pro Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala 275 280 285		
Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala 290 295 300		
Leu Gln Ala Val Ser Glu Gln Glu Lys Thr Val Glu Glu Val Pro His 305 310 315 320		
Pro Leu Asp Arg Asp Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu 325 330 335		
Asp Ser Gly Ala Pro Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln 340 345 350		
Thr Gly Ser Asn His Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val 355 360 365		
Asn Gln Glu Gly Glu Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly 370 375 380		
Asn Arg Lys Leu Leu Trp His Gly Thr Asn Met Ala Val Val Ala Ala 385 390 395 400		
Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser Gly Gly Arg Val 405 410 415		
Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr 420 425 430		
Val Ile Gly Met Lys Cys Gly Ala His His Val Gly Tyr Met Phe Leu 435 440 445		
Gly Glu Val Ala Leu Gly Arg Glu His His Ile Asn Thr Asp Asn Pro 450 455 460		
Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly 465 470 475 480		

His	Thr	Glu	Pro	Asp	Pro	Thr	Gln	Asp	Thr	Glu	Leu	Glu	Leu	Asp	Gly
				485					490					495	
Gln	Gln	Val	Val	Val	Pro	Gln	Gly	Gln	Pro	Val	Pro	Cys	Pro	Glu	Phe
			500					505					510		
Ser	Ser	Ser	Thr	Phe	Ser	Gln	Ser	Glu	Tyr	Leu	Ile	Tyr	Gln	Glu	Ser
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Met Ala
1

cca aaa cga aag gcc tct gtg cag act gag ggc tcc aag aag cag cga 165
Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg
5 10 15

caa ggg aca gag gag gag gac agc ttc cgg tcc act gcc gag gct ctc 213
Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu Ala Leu
20 25 30

aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc tca tgt 261
Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys
35 40 45 50

cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat gac tgt 309
Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys
55 60 65

acc ctg aac cag acc aac atc ggc aac aac aac aac aag ttc tat att 357
Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe Tyr Ile
70 75 80

atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat cgc tgg 405
Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn Arg Trp
85 90 95

ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc acc tgc	453
Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys	
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ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag aag act	501
Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu Lys Thr	
115 120 125 130	
aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc aac aag	549
Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys	
135 140 145	
tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag gct gta	597
Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu Ala Val	
150 155 160	
gtg aag gcc tta tct ccc cag gtg gac agc ggc cct gtg agg acc gtg	645
Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg Thr Val	
165 170 175	
gtc aag ccc tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac	693
Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn	
180 185 190	
atc ttc agc aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg	741
Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu	
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gat gtg aag aag atg ccc ttg gga aag ctg acc aag cag cag att gcc	789
Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala	
215 220 225	
cgt ggc ttc gag gcc ttg gaa gct cta gag gag gcc atg aaa aac ccc	837
Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro	
230 235 240	
aca ggg gat ggc cag agc ctg gaa gag ctc tcc tcc tgc ttc tac act	885
Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr	
245 250 255	
gtc atc cca cac aac ttc ggc cgc agc cga ccc ccg ccc atc aac tcc	933
Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser	
260 265 270	
cct gat gtg ctt cag gcc aag aag gac atg ctg ctg gtg cta gcg gac	981
Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp	
275 280 285 290	
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Il Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu	
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Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu	
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Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala	
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Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn	
340 345 350	
ctg cgg cat gtt tgg aaa gtg aac cga gaa ggg gag gga gac agg ttc	1221
Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe	
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Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr	
375 380 385	
aat gtg gcc gtg gtg gct gcc atc ctc acc agt ggg ctc cga atc atg	1317
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390 395 400	
cca cac tcg ggt ggt cgt gtt ggc aag ggt att tat ttt gcc tct gag	1365
Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu	
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Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His	
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Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His	
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Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro	
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Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu	
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Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu	

515

520

525

530

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1740

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<212> PRT

<213> Mus musculus

<400> 8

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 35 40 45

Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr
 50 55 60

Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe
 65 70 75 80

Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn
 85 90 95

Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe
 100 105 110

Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu
 115 120 125

Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro
 130 135 140

Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu
 145 150 155 160

Ala Val Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg
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Thr Val Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile
 180 185 190

Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met
 195 200 205

Asn Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln

Asn Pro Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe
245 250 255

Asn Ser Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu
275 280 285

Glu Glu Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln
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Leu Leu Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr
325 330 335

Lys Ala Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys
340 345 350

Pro Asn Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp
355 360 365

Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His
370 375 380

Gly Thr Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg
385 390 395 400

Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
405 410 415

Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly
420 425 430

Gly His Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys
435 440 445

Glu His His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro
450 455 460

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Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu	
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gct ctc aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc	144
Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro	
35 40 45	
tca tgt cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat	192
Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr	
50 55 60	
gac tgt acc ctg aac cag acc aac atc ggc aac aac aac aac aag ttc	240
Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe	
65 70 75 80	
tat att atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat	288
Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn	
85 90 95	
cgc tgg ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc	336
Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe	
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acc tgc ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag	384
Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu	
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Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro	
130 135 140	
aac aag tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag	480
Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu	
145 150 155 160	
gct gta gtg aag gtg gac agc ggc cct gtg agg acc gtg gtc aag ccc	528
Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro	
165 170 175	
tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac atc ttc agc	576
Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser	
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aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg gat gtg aag	624
Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys	
195 200 205	
aag atg ccc ttg gga aag ctg acc aag cag cag att gcc cgt ggc ttc	672
Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe	
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Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp	
225 230 235 240	
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Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro	
245 250 255	
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His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val	
260 265 270	
ctt cag gcc aag aag gac atg ctg ctg gtg cta gcg gac atc gag ttg	864
Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu	
275 280 285	
gcg cag acc ttg cag gca gcc cct ggg gag gag gag gag aaa gtg gaa	912
Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu Lys Val Glu	
290 295 300	
gag gtg cca cac cca ctg gat cga gac tac cag ctc ctc agg tgc cag	960
Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln	
305 310 315 320	
ctt caa ctg ctg gac tcc ggg gag tcc gag tac aag gca ata cag acc	1008
Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr	
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tac ctg aaa cag act ggc aac agc tac agg tgc cca aac ctg cgg cat	1056

Tyr	Leu	Lys	Gln	Thr	Gly	Asn	Ser	Tyr	Arg	Cys	Pro	Asn	Leu	Arg	His	
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Val	Trp	Lys	Val	Asn	Arg	Glu	Gly	Glu	Gly	Asp	Arg	Phe	Gln	Ala	His	
		355					360					365				
tcc	aaa	ctg	ggc	aat	cgg	agg	ctg	ctg	tgg	cac	ggc	acc	aat	gtg	gcc	1152
Ser	Lys	Leu	Gly	Asn	Arg	Arg	Leu	Leu	Trp	His	Gly	Thr	Asn	Val	Ala	
		370				375					380					
gtg	gtg	gct	gcc	atc	ctc	acc	agt	ggg	ctc	cga	atc	atg	cca	cac	tcg	1200
Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met	Pro	His	Ser	
		385				390				395					400	
ggg	ggg	cgt	gtt	ggc	aag	ggg	att	tat	ttt	gcc	tct	gag	aac	agc	aag	1248
Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala	Ser	Glu	Asn	Ser	Lys	
				405					410					415		
tca	gct	ggc	tat	gtt	acc	acc	atg	cac	tgt	ggg	ggc	cac	cag	gtg	ggc	1296
Ser	Ala	Gly	Tyr	Val	Thr	Thr	Met	His	Cys	Gly	Gly	His	Gln	Val	Gly	
			420					425					430			
tac	atg	ttc	ctg	ggc	gag	gtg	gcc	ctc	ggc	aaa	gag	cac	cac	atc	acc	1344
Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly	Lys	Glu	His	His	Ile	Thr	
		435				440					445					
atc	gat	gac	ccc	agc	ttg	aag	agt	cca	ccc	cct	ggc	ttt	gac	agc	gtc	1392
Ile	Asp	Asp	Pro	Ser	Leu	Lys	Ser	Pro	Pro	Pro	Gly	Phe	Asp	Ser	Val	
		450				455					460					
atc	gcc	cga	ggc	caa	acc	gag	ccg	gat	ccc	gcc	cag	gac	att	gaa	ctt	1440
Ile	Ala	Arg	Gly	Gln	Thr	Glu	Pro	Asp	Pro	Ala	Gln	Asp	Ile	Glu	Leu	
		465				470				475					480	
gaa	ctg	gat	ggg	cag	ccg	gtg	gtg	gtg	ccc	caa	ggc	ccg	cct	gtg	cag	1488
Glu	Leu	Asp	Gly	Gln	Pro	Val	Val	Val	Pro	Gln	Gly	Pro	Pro	Val	Gln	
			485						490					495		
tgc	ccg	tca	ttc	aaa	agc	tcc	agc	ttc	agc	cag	agt	gaa	tac	ctc	ata	1536
Cys	Pro	Ser	Phe	Lys	Ser	Ser	Ser	Phe	Ser	Gln	Ser	Glu	Tyr	Leu	Ile	
			500					505					510			
tac	aag	gag	agc	cag	tgt	cgc	ctg	cgc	tac	ctg	ctg	gag	att	cac	ctc	1584
Tyr	Lys	Glu	Ser	Gln	Cys	Arg	Leu	Arg	Tyr	Leu	Leu	Glu	Ile	His	Leu	
		515				520						525				
taa																1587

<210> 10
 <211> 528
 <212> PRT

<213> Mus musculus

<400> 10

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys
 1 5 10 15

Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu
 20 25 30

Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro
 35 40 45

Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr
 50 55 60

Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe
 65 70 75 80

Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn
 85 90 95

Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe
 100 105 110

Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu
 115 120 125

Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro
 130 135 140

Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu
 145 150 155 160

Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro
 165 170 175

Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser
 180 185 190

Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys
 195 200 205

Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe
 210 215 220

Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp
 225 230 235 240

Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro
 245 250 255

His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val

260					265					270					
Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	Val	Leu	Ala	Asp	Il	Glu	Leu
	275						280					285			
Ala	Gln	Thr	Leu	Gln	Ala	Ala	Pro	Gly	Glu	Glu	Glu	Glu	Lys	Val	Glu
	290					295					300				
Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln	Leu	Leu	Arg	Cys	Gln
305					310					315					320
Leu	Gln	Leu	Leu	Asp	Ser	Gly	Glu	Ser	Glu	Tyr	Lys	Ala	Ile	Gln	Thr
				325					330					335	
Tyr	Leu	Lys	Gln	Thr	Gly	Asn	Ser	Tyr	Arg	Cys	Pro	Asn	Leu	Arg	His
			340					345					350		
Val	Trp	Lys	Val	Asn	Arg	Glu	Gly	Glu	Gly	Asp	Arg	Phe	Gln	Ala	His
	355						360					365			
Ser	Lys	Leu	Gly	Asn	Arg	Arg	Leu	Leu	Trp	His	Gly	Thr	Asn	Val	Ala
	370					375					380				
Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met	Pro	His	Ser
385					390					395					400
Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala	Ser	Glu	Asn	Ser	Lys
				405					410					415	
Ser	Ala	Gly	Tyr	Val	Thr	Thr	Met	His	Cys	Gly	Gly	His	Gln	Val	Gly
		420						425					430		
Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly	Lys	Glu	His	His	Ile	Thr
	435						440					445			
Ile	Asp	Asp	Pro	Ser	Leu	Lys	Ser	Pro	Pro	Pro	Gly	Phe	Asp	Ser	Val
	450					455					460				
Ile	Ala	Arg	Gly	Gln	Thr	Glu	Pro	Asp	Pro	Ala	Gln	Asp	Ile	Glu	Leu
465					470					475					480
Glu	Leu	Asp	Gly	Gln	Pro	Val	Val	Val	Pro	Gln	Gly	Pro	Pro	Val	Gln
				485					490					495	
Cys	Pro	Ser	Phe	Lys	Ser	Ser	Ser	Phe	Ser	Gln	Ser	Glu	Tyr	Leu	Ile
			500					505					510		
Tyr	Lys	Glu	Ser	Gln	Cys	Arg	Leu	Arg	Tyr	Leu	Leu	Glu	Ile	His	Leu
	515						520					525			

<210> 11

<211> 18

<212> PRT
 <213> artificial sequence

<220>
 <223> NAD+ binding domain

<220>
 <221> VARIANT
 <222> (2)...(6), (9)...(11)
 <223> any amino acid; residues 3 to 6 may be present or absent

<220>
 <221> VARIANT
 <222> (7)
 <223> amino acid residue 7 is either Ser or Thr

<400> 11

Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Gly	Lys	Gly	Ile	Tyr
1				5				10						15	

Phe Ala

<210> 12
 <211> 25
 <212> PRT
 <213> artificial sequence

<220>
 <223> NAD+ binding domain

<220>
 <221> VARIANT
 <222> (1), (14)
 <223> amino acid residues 1 and 14 are either Ser or Thr

<220>
 <221> VARIANT
 <222> (2), (7), (9)...(13), (16)...(18)
 <223> may be any amino acid; 10-13 may be present or absent

<220>
 <221> VARIANT
 <222> (6)
 <223> amino acid residue 6 is either Ile or Val

<400> 12

Xaa	Xaa	Gly	Leu	Arg	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa
1				5				10						15	

Xaa Xaa Gly Lys Gly Ile Tyr Phe Ala

20

25

<210> 13
 <211> 49
 <212> PRT
 <213> artificial sequence

<220>
 <223> NAD+ binding domain

<220>
 <221> VARIANT
 <222> (6), (16), (29)
 <223> Ser or Thr

<220>
 <221> VARIANT
 <222> (7)...(13), (17), (22), (24)...(28), (31)...(33), (41)...(43), (48)
 <223> may be any amino acid; residues 25-28 may be present or absent

<220>
 <221> VARIANT
 <222> 21
 <223> Ile or Val

<400> 13

Leu Leu Trp His Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Leu Xaa
 1 5 10 15

Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
 20 25 30

Xaa Gly Lys Gly Ile Tyr Phe Ala Xaa Xaa Xaa Ser Lys Ser Ala Xaa
 35 40 45

Tyr

<210> 14
 <211> 22
 <212> PRT
 <213> artificial sequence

<220>
 <223> leucine zipper motif

<220>
 <221> VARIANT
 <222> (1)
 <223> Leu or Val

<220>
 <221> VARIANT
 <222> (2)...(7), (9)...(14), (16)...(21)
 <223> may be any amino acid

<400> 14

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu
 20

<210> 15
 <211> 37
 <212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 1

<220>
 <221> VARIANT
 <222> (21)
 <223> Asp or Glu

<220>
 <221> VARIANT
 <222> (2)...(10), (12)...(13), (15)...(16), (20), (22)...(32)
 <223> may be any amino acid; residue 32 may be present or absent

<400> 15

Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Tyr Xaa Xaa
 1 5 10 15

Gln Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Trp Gly Arg Val Gly
 35

<210> 16
 <211> 29
 <212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 2

<220>

<221> VARIANT

<222> (2)...(4), (6), (8)...(11), (14), (16), (18)...(22), (24)...(26), (28)

<223> may be any amino acid

<400> 16

Ala Xaa Xaa Xaa Phe Xaa Lys Xaa Xaa Xaa Xaa Lys Thr Xaa Asn Xaa
1 5 10 15

Trp Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Pro Xaa Lys
20 25

<210> 17

<211> 44

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 3

<220>

<221> VARIANT

<222> (2), (5)...(6), (8)...(16), (18)...(27), (33)...(35), (38)...(43)

<223> may be any amino acid

<220>

<221> VARIANT

<222> (4)

<223> Ile or Leu

<400> 17

Gln Xaa Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Leu Gly Lys Leu
20 25 30

Xaa Xaa Xaa Gln Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu
35 40

<210> 18

<211> 15

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 4

<220>

<221> VARIANT

<222> (4), (8), (11)...(13)
 <223> may be any amino acid

<400> 18

Phe	Tyr	Thr	Xaa	Ile	Pro	His	Xaa	Phe	Gly	Xaa	Xaa	Xaa	Pro	Pro
1				5					10				15	

<210> 19
 <211> 17
 <212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 5

<220>
 <221> VARIANT
 <222> (2)...(4), (6)...(7), (9), (13), (15)...(16)
 <223> may be any amino acid

<400> 19

Lys	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Leu	Xaa	Asp	Ile	Glu	Xaa	Ala	Xaa	Xaa
1				5					10				15		

Leu

<210> 20
 <211> 11
 <212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 6

<220>
 <221> VARIANT
 <222> (2)...(4), (6)
 <223> may be any amino acid

<400> 20

Gly	Xaa	Xaa	Xaa	Leu	Xaa	Glu	Val	Ala	Leu	Gly
1				5					10	

<210> 21
 <211> 28

<212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 7

<220>
 <221> VARIANT
 <222> (2)...(3), (5)...(8), (10)...(12), (14)...(22), (24), (26)...(27)
 <223> may be any amino acid; residues 21 and 22 may be present or absent

<400> 21

Gly Xaa Xaa Ser Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Gly Xaa Xaa Val
 20 25

<210> 22
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 8

<220>
 <221> VARIANT
 <222> (2)
 <223> Tyr or Phe

<220>
 <221> VARIANT
 <222> (3)...(4), (6)...(8), (10)...(13)
 <223> may be any amino acid

<400> 22

Glu Xaa Xaa Xaa Tyr Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Tyr Leu Leu
 1 5 10 15

<210> 23
 <211> 20
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 23

Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala
 1 5 10 15

Leu Asn Glu Ser
 20

<210> 24
 <211> 20
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 24

Lys Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg
 1 5 10 15

Asn Leu His Cys
 20

<210> 25
 <211> 21
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 25

Cys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr
 1 5 10 15

Ala Glu Ala Leu Lys
 20

<210> 26
 <211> 20
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 26

Cys Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu
 1 5 10 15

Glu Ala Leu Lys
20

<210> 27
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> synthetic sequence for antibody production

<400> 27

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
1 5 10 15

Ala Leu Lys

<210> 28
<211> 19
<212> PRT
<213> Mus musculus

<400> 28

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
1 5 10 15

Ala Met Lys

<210> 29
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> NAD⁺ binding domain

<220>
<221> VARIANT
<222> (2)...(4)
<223> may be any amino acid residue

<400> 29

Gly Xaa Xaa Xaa Gly Lys Gly
1 5

<210> 30

<211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PARP zinc finger sequence motif

<220>
 <221> VARIANT
 <222> (2)...(3), (5)...(34), (36)...(37)
 <223> may be any amino acid; residues 33 and 34 may be present or absent

<400> 30

Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa His Xaa Xaa Cys
 35

<210> 31
 <211> 10
 <212> PRT
 <213> Arabidopsis thaliana

<400> 31

Ala Ala Val Leu Asp Gln Trp Ile Pro Asp
 1 5 10

<210> 32
 <211> 39
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(39)

<400> 32

gta tgc cag gaa ggt cat ggg cca gca aaa ggg tct ctg
 Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
 1 5 10

39

<210> 33
 <211> 13

<212> PRT

<213> Homo sapiens

<400> 33

Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
1 5 10
